CLAIMS

What is claimed is:

1. A method of inhibiting the ability of a cell to degrade an extracellular matrix, the method comprising inhibiting the activity of 22437 protein expressed by the cell, whereby the ability of the cell to degrade the extracellular matrix is inhibited.

2. The method of claim 1, wherein the activity of 22437 protein expressed by the cell is inhibited by inhibiting expression of the 22437 gene in the cell.

3. The method of claim 2, wherein expression of the 22437 gene is inhibited by administering to the cell an antisense oligonucleotide which hybridizes under stringent conditions with a transcript of the 22437 gene.

4. The method of claim 3, wherein the antisense oligonucleotide comprises at least 15 nucleotide residues.

5. The method of claim 3, wherein the transcript is an mRNA.

6. The method of claim 2, wherein expression of the 22437 gene is inhibited by administering to the cell an antisense oligonucleotide which hybridizes under stringent conditions with a polynucleotide having the nucleotide sequence SEQ ID NO: 1.

7. The method of claim 2, wherein expression of the 22437 gene is inhibited by administering to the cell an antisense oligonucleotide which hybridizes under stringent conditions with a polynucleotide having the nucleotide sequence SEQ ID NO: 3.

8. The method of claim 1, wherein the activity of 22437 protein expressed by the cell is inhibited by inhibiting a catalytic activity of 22437 protein without significantly affecting 22437 gene expression in the cell.

9. The method of claim 1, wherein the activity of 22437 is inhibited by administering to the cell an agent which inhibits an activity of 22437 protein.

10. The method of claim 9, wherein the agent is an antibody which specifically binds with 22437 protein.

11. The method of claim 9, wherein the activity is sulfatase activity.

12. The method of claim 9, wherein the activity is ability to degrade an extracellular matrix.

13. The method of claim 1, wherein the cell is a tumor cell.

14. The method of claim 13, wherein the tumor cell is selected from the group consisting of a colon tumor cell, an ovarian cancer cell, a breast cancer cell, a lung cancer cell, and a glioblastoma cell.

15. The method of claim 1, wherein the cell is a vascular endothelial cell.

16. The method of claim 1, wherein the cell is a neuronal cell.

17. The method of claim 16, wherein the neuronal cell is selected from the group consisting of an astrocyte, a neuron of the cerebral cortex, and a neuron of the hypothalamus.

18. The method of claim 1, wherein the cell is in the body of a human.

19. A method for assessing whether a test compound is useful for modulating at least one phenomenon selected from the group consisting of tumor establishment, tumor

growth, tumor metastasis, epithelial cell proliferation, endothelial cell proliferation, neuronal cell growth, wound healing, and cerebral injury healing, the method comprising:

a) adding the test compound to a first composition comprising a polypeptide that has an amino acid sequence at least 80% identical to SEQ ID NO: 2 and that exhibits a 22437 activity and;

b) comparing the 22437 activity in the first composition and 22437 activity in a second composition that is substantially identical to the first, except that it does not comprise the test compound,

whereby a difference in 22437 activity in the first and second compositions is an indication that the test compound is useful for modulating the phenomenon.

20. The method of claim 19, wherein the activity is selected from the group consisting of sulfatase activity and ability to degrade an extracellular matrix.

21. The method of claim 19, wherein the protein has the amino acid sequence SEQ ID NO: 2.

22. The method of claim 19, wherein the first composition comprises a cell comprising a nucleic acid encoding the protein.

23. The method of claim 22, wherein the nucleic acid is the genome of the cell.

24. The method of claim 22, wherein the nucleic acid comprises the 22437 gene

25. A method for assessing whether a test compound is useful for modulating at least one phenomenon selected from the group consisting of tumor establishment, tumor growth, tumor metastasis, epithelial cell proliferation, endothelial cell proliferation, neuronal cell growth, wound healing, and cerebral injury healing, the method comprising:

a) adding the test compound to a first composition comprising a cell which comprises a nucleic acid that encodes a polypeptide that has an amino acid sequence at least 80% identical to SEQ ID NO: 2 and that exhibits a 22437 activity and;

b) comparing 22437 activity in the first composition and 22437 activity in a second composition that is substantially identical to the first composition, except that it does not comprise the test compound,

whereby a difference in 22437 activity in the first and second compositions is an indication that the test compound is useful for modulating the phenomenon.

26. A method of making a pharmaceutical composition for modulating at least one phenomenon selected from the group consisting of tumor establishment, tumor growth, tumor metastasis, epithelial cell proliferation, endothelial cell proliferation, neuronal cell growth, wound healing, and cerebral injury healing, the method comprising:

a) selecting a test compound useful for modulating the phenomenon according to the method of claim 19; and

b) combining the test compound with a pharmaceutically acceptable carrier in order to make the pharmaceutical composition.

27. A method of modulating, in a human, at least one phenomenon selected from the group consisting of tumor establishment, tumor growth, tumor metastasis, epithelial cell proliferation, endothelial cell proliferation, neuronal cell growth, wound healing, and cerebral injury healing, the method comprising administering the pharmaceutical composition of claim 26 to the human in an amount effective to modulate the phenomenon.

28. A method for identifying a compound useful for modulating at least one phenomenon selected from the group consisting of tumor establishment, tumor growth, tumor metastasis, epithelial cell proliferation, endothelial cell proliferation, neuronal cell growth, wound healing, and cerebral injury healing, the method comprising:

a) contacting the test compound and a polypeptide selected from the group consisting of

i) a polypeptide which is encoded by a nucleic acid molecule comprising a portion having a nucleotide sequence which is at least 60% identical to either of SEQ ID NOs: 1 and 3; and

ii) a fragment of a polypeptide having either an amino acid sequence comprising SEQ ID NO: 2, wherein the fragment comprises at least 15 contiguous amino acid residues of SEQ ID NO: 2

or a cell that expresses the polypeptide; and

b) determining whether the polypeptide binds with the test compound, whereby binding of the polypeptide and the test compound is an indication that the test compound is useful for modulating the phenomenon.

29. The method of claim 28, wherein the polypeptide exhibits an activity selected from the group consisting of sulfatase activity and ability to degrade an extracellular matrix.

30. The method of claim 28, wherein the polypeptide exhibits an epitope in common with a polypeptide having the amino acid sequence SEQ ID NO: 2.

SEQUENCE LISTING

<110> GLUCKSMANN, Maria A.
MEYERS, Rachel
KAPELLER-LIBERMANN, Rosana
SILOS-SANTIAGO, Inmaculada

<120> 22437, A NOVEL HUMAN SULFATASE AND USES THEREFOR

<130> 10147-61U1

<140> NOT YET ASSIGNED
<141> 2001-10-03

<150> US 60/257,082
<151> 2000-12-21.

<160> 12

<170> PatentIn Ver. 2.1

<210> 1
<211> 3513
<212> DNA
<213> Homo sapiens

<400> 1
cgcgtccggg cagattcacg tcgtttccag ccaagtggac ctgatcgatg gccctcctga 60
atttatcacg atatttgatt tattagcgat gccccctggt ttgtgtgtta cgcacacaca 120
cgtgcacaca aggctctggc tcgcttccct ccctcgtttc cagctcctgg gcgaatccca 180
catctgtttc aactctccgc cgagggcgag caggagcgag agtgtgtcga atctgcgagt 240
gaagagggac gagggaaaag aaacaaagcc acagacgcaa cttgagactc ccgcatccca 300
aaagaagcac cagatcagca aaaaaagaag atgggccccc cgagcctcgt gctgtgcttg 360
ctgtccgcaa ctgtgttctc cctgctgggt ggaagctcgg ccttcctgtc gcaccaccgc 420
ctgaaaggca ggtttcagag ggaccgcagg aacatccgcc ccaacatcat cctggtgctg 480
acggacgacc aggatgtgga gctgggttcc atgcaggtga tgaacaagac ccggcgcatc 540
atggagcagg gcgggacgca cttcatcaac gccttcgtga ccacacccat gtgctgcccc 600
tcacgctcct ccatcctcac cggcaagtac gtccacaacc acaacaccta caccaacaat 660
gagaactgct cctcgccctc ctggcaggca cagcacgaga gccgcacctt tgccgtgtac 720
ctcaatagca ctggctaccg gacagctttc ttcgggaagt atcttaatga atacaacggc 780
tcctacgtgc cacccggctg gaaggagtgg gtcggactcc ttaaaaactc ccgcttttat 840
aactacacgc tgtgtcggaa cggggtgaaa gagaagcacg gctccgacta ctccaaggat 900
tacctcacag acctcatcac caatgacagc gtgagcttct tccgcacgtc caagaagatg 960
tacccgcaca ggccagtcct catggtcatc agccatgcag ccccccacgg ccctgaggat 1020
tcagccccac aatattcacg cctcttccca aacgcatctc agcacatcac gccgagctac 1080
aactacgcgc ccaacccgga caaacactgg atcatgcgct acacggggcc catgaagccc 1140
atccacatgg aattcaccaa catgctccag cggaagcgct tgcagaccct catgtcggtg 1200
gacgactcca tggagacgat ttacaacatg ctggttgaga cgggcgagct ggacaacacg 1260

tacatcgtat acaccgccga ccacggttac cacatcggcc agtttggcct ggtgaaaggg 1320
aaatccatgc catatgagtt tgacatcagg gtcccgttct acgtgagggg ccccaacgtg 1380
gaagccggct gtctgaatcc ccacatcgtc ctcaacattg acctggcccc caccatcctg 1440
gacattgcag gcctggacat acctgcggat atggacggga aatccatcct caagctgctg 1500
gacacggagc ggccggtgaa tcggtttcac ttgaaaaaga agatgagggt ctggcgggac 1560
tccttcttgg tggagagagg caagctgcta cacaagagag acaatgacaa ggtggacgcc 1620
caggaggaga actttctgcc caagtaccag cgtgtgaagg acctgtgtca gcgtgctgag 1680
taccagacgg cgtgtgagca gctgggacag aagtggcagt gtgtggagga cgccacgggg 1740
aagctgaagc tgcataagtg caagggcccc atgcggctgg gcggcagcag agccctctcc 1800
aacctcgtgc ccaagtacta cgggcagggc agcgaggcct gcacctgtga cagcggggac 1860
tacaagctca gcctggccgg acgccggaaa aaactcttca agaagaagta caaggccagc 1920
tatgtccgca gtcgctccat ccgctcagtg gccatcgagg tggacggcag ggtgtaccac 1980
gtaggcctgg gtgatgccgc ccagccccga aacctcacca agcggcactg gccaggggcc 2040
cctgaggacc aagatgacaa ggatggtggg gacttcagtg gcactggagg ccttcccgac 2100
tactcagccg ccaaccccat taaagtgaca catcggtgct acatcctaga gaacgacaca 2160
gtccagtgtg acctggacct gtacaagtcc ctgcaggcct ggaaagacca caagctgcac 2220
atcgaccacg agattgaaac cctgcagaac aaaattaaga acctgaggga agtccgaggt 2280
cacctgaaga aaaagcggcc agaagaatgt gactgtcaca aaatcagcta ccacacccag 2340
cacaaaggcc gcctcaagca cagaggctcc agtctgcatc ctttcaggaa gggcctgcaa 2400
gagaaggaca aggtgtggct gttgcgggag cagaagcgca agaagaaact ccgcaagctg 2460
ctcaagcgcc tgcagaacaa cgacacgtgc agcatgccag gcctcacgtg cttcacccac 2520
gacaaccagc actggcagac ggcgcctttc tggacactgg ggcctttctg tgcctgcacc 2580
agcgccaaca ataacacgta ctggtgcatg aggaccatca atgagactca caatttcctc 2640
ttctgtgaat ttgcaactgg cttcctagag tactttgatc tcaacacaga cccctaccag 2700
ctgatgaatg cagtgaacac actggacagg gatgtcctca accagctaca cgtacagctc 2760
atggagctga ggagctgcaa gggttacaag cagtgtaacc cccggactcg aaacatggac 2820
ctgggactta aagatggagg aagctatgag caatacaggc agtttcagcg tcgaaagtgg 2880
ccagaaatga agagaccttc ttccaaatca ctgggacaac tgtgggaagg ctgggaaggt 2940
taagaaacaa cagaggtgga cctccaaaaa catagaggca tcacctgact gcacaggcaa 3000
tgaaaaacca tgtgggtgat ttccagcaga cctgtgctat tggccaggag gcctgagaaa 3060
gcaagcacgc actctcagtc aacatgacag attctggagg ataaccagca ggagcagaga 3120
taacttcagg aagtccattt ttgcccctgc ttttgctttg gattatacct caccagctgc 3180
acaaaatgca ttttttcgta tcaaaaagtc accactaacc ctccccccaga agctcacaaa 3240
ggaaaacgga gagagcgagc gagagagatt tccttggaaa tttctcccaa gggcgaaagt 3300
cattggaatt tttaaatcat aggggaaaag cagtcctgtt ctaaatcctc ttattctttt 3360
ggtttgtcac aaagaaggaa ctaagaagca ggacagaggc aacgtggaga ggctgaaaac 3420
agtgcagaga cgtttgacaa tgagtcagta gcacaaaaga gatgacattt acctagcact 3480
ataaaccctg gttgcctctg aagaaactgc ctt 3513

<210> 2
<211> 870
<212> PRT
<213> Homo sapiens

<400> 2
Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
1 5 10 15

Ser Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Leu Lys
20 25 30

Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn Ile Ile Leu
35 40 45

Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Met Gln Val Met
50 55 60

Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly Thr His Phe Ile Asn
65 70 75 80

Ala Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Ile Leu
85 90 95

Thr Gly Lys Tyr Val His Asn His Asn Thr Tyr Thr Asn Asn Glu Asn
100 105 110

Cys Ser Ser Pro Ser Trp Gln Ala Gln His Glu Ser Arg Thr Phe Ala
115 120 125

Val Tyr Leu Asn Ser Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr
130 135 140

Leu Asn Glu Tyr Asn Gly Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp
145 150 155 160

Val Gly Leu Leu Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg
165 170 175

Asn Gly Val Lys Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu
180 185 190

Thr Asp Leu Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys
195 200 205

Lys Met Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala
210 215 220

Pro His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
225 230 235 240

Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Pro
245 250 255

Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro Ile His
260 265 270

Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln Thr Leu Met
275 280 285

Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met Leu Val Glu Thr
290 295 300

Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr
305 310 315 320

His Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Glu
325 330 335

Phe Asp Ile Arg Val Pro Phe Tyr Val Arg Gly Pro Asn Val Glu Ala
340 345 350

Gly Cys Leu Asn Pro His Ile Val Leu Asn Ile Asp Leu Ala Pro Thr
355 360 365

Ile Leu Asp Ile Ala Gly Leu Asp Ile Pro Ala Asp Met Asp Gly Lys
370 375 380

Ser Ile Leu Lys Leu Leu Asp Thr Glu Arg Pro Val Asn Arg Phe His
385 390 395 400

Leu Lys Lys Lys Met Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg
405 410 415

Gly Lys Leu Leu His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu
420 425 430

Glu Asn Phe Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg
435 440 445

Ala Glu Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys
450 455 460

Val Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro
465 470 475 480

Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr
485 490 495

Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys
500 505 510

Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Lys Tyr Lys
515 520 525

Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val
530 535 540

Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg
545 550 555 560

Asn Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp
565 570 575

Lys Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser
580 585 590

Ala Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn
595 600 605

Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp
610 615 620

Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn
625 630 635 640

Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg
645 650 655

Pro Glu Glu Cys Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys
660 665 670

Gly Arg Leu Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly
675 680 685

Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys
690 695 700

Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
705 710 715 720

Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln
725 730 735

Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala
740 745 750

Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn
755 760 765

Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu
770 775 780

Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg
785 790 795 800

Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys
805 810 815

Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly
820 825 830

Leu Lys Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg
835 840 845

Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu
850 855 860

Trp Glu Gly Trp Glu Gly
865 870

<210> 3
<211> 2610
<212> DNA
<213> Homo sapiens

<400> 3
atgggccccc cgagcctcgt gctgtgcttg ctgtccgcaa ctgtgttctc cctgctgggt 60
ggaagctcgg ccttcctgtc gcaccaccgc ctgaaaggca ggtttcagag ggaccgcagg 120
aacatccgcc ccaacatcat cctggtgctg acggacgacc aggatgtgga gctgggttcc 180
atgcaggtga tgaacaagac ccggcgcatc atggagcagg gcgggacgca cttcatcaac 240
gccttcgtga ccacacccat gtgctgcccc tcacgctcct ccatcctcac cggcaagtac 300
gtccacaacc acaacaccta caccaacaat gagaactgct cctcgccctc ctggcaggca 360
cagcacgaga gccgcacctt tgccgtgtac ctcaatagca ctggctaccg gacagctttc 420
ttcgggaagt atcttaatga atacaacggc tcctacgtgc cacccggctg gaaggagtgg 480
gtcggactcc ttaaaaactc ccgcttttat aactacacgc tgtgtcggaa cggggtgaaa 540
gagaagcacg gctccgacta ctccaaggat tacctcacag acctcatcac caatgacagc 600
gtgagcttct tccgcacgtc caagaagatg tacccgcaca ggccagtcct catggtcatc 660
agccatgcag ccccccacgg ccctgaggat tcagccccac aatattcacg cctcttccca 720
aacgcatctc agcacatcac gccgagctac aactacgcgc ccaacccgga caaacactgg 780
atcatgcgct acacggggcc catgaagccc atccacatgg aattcaccaa catgctccag 840
cggaagcgct tgcagaccct catgtcggtg gacgactcca tggagacgat ttacaacatg 900
ctggttgaga cgggcgagct ggacaacacg tacatcgtat acaccgccga ccacggttac 960
cacatcggcc agtttggcct ggtgaaaggg aaatccatgc catatgagtt tgacatcagg 1020
gtcccgttct acgtgagggg ccccaacgtg gaagccggct gtctgaatcc ccacatcgtc 1080
ctcaacattg acctggcccc caccatcctg gacattgcag gcctggacat acctgcggat 1140
atggacggga aatccatcct caagctgctg gacacggagc ggccggtgaa tcggtttcac 1200
ttgaaaaaga agatgagggt ctggcgggac tccttcttgg tggagagagg caagctgcta 1260
cacaagagag acaatgacaa ggtggacgcc caggaggaga actttctgcc caagtaccag 1320

cgtgtgaagg acctgtgtca gcgtgctgag taccagacgg cgtgtgagca gctgggacag 1380
aagtggcagt gtgtggagga cgccacgggg aagctgaagc tgcataagtg caagggcccc 1440
atgcggctgg gcggcagcag agccctctcc aacctcgtgc ccaagtacta cgggcagggc 1500
agcgaggcct gcacctgtga cagcggggac tacaagctca gcctggccgg acgccggaaa 1560
aaactcttca agaagaagta caaggccagc tatgtccgca gtcgctccat ccgctcagtg 1620
gccatcgagg tggacggcag ggtgtaccac gtaggcctgg gtgatgccgc ccagccccga 1680
aacctcacca agcggcactg gccaggggcc cctgaggacc aagatgacaa ggatggtggg 1740
gacttcagtg gcactggagg ccttcccgac tactcagccg ccaaccccat taaagtgaca 1800
catcggtgct acatcctaga gaacgacaca gtccagtgtg acctggacct gtacaagtcc 1860
ctgcaggcct ggaaagacca caagctgcac atcgaccacg agattgaaac cctgcagaac 1920
aaaattaaga acctgaggga agtccgaggt cacctgaaga aaaagcggcc agaagaatgt 1980
gactgtcaca aaatcagcta ccacacccag cacaaaggcc gcctcaagca cagaggctcc 2040
agtctgcatc ctttcaggaa gggcctgcaa gagaaggaca aggtgtggct gttgcgggag 2100
cagaagcgca agaagaaact ccgcaagctg ctcaagcgcc tgcagaacaa cgacacgtgc 2160
agcatgccag gcctcacgtg cttcacccac gacaaccagc actggcagac ggcgcctttc 2220
tggacactgg ggcctttctg tgcctgcacc agcgccaaca ataacacgta ctggtgcatg 2280
aggaccatca atgagactca caatttcctc ttctgtgaat ttgcaactgg cttcctagag 2340
tactttgatc tcaacacaga cccctaccag ctgatgaatg cagtgaacac actggacagg 2400
gatgtcctca accagctaca cgtacagctc atggagctga ggagctgcaa gggttacaag 2460
cagtgtaacc cccggactcg aaacatggac ctgggactta aagatggagg aagctatgag 2520
caatacaggc agtttcagcg tcgaaagtgg ccagaaatga agagaccttc ttccaaatca 2580
ctgggacaac tgtgggaagg ctgggaaggt 2610

<210> 4
<400> 4
000

<210> 5
<400> 5
000

<210> 6
<400> 6
000

<210> 7
<400> 7
000

<210> 8
<400> 8
000

<210> 9
<400> 9
000

<210> 10
<400> 10
000

<210> 11
<211> 4397
<212> DNA
<213> Homo sapiens

<400> 11
gagcgagagt gtgtcgagtg agtgtgcgtc tgtgtgtccc ggcgagggtg cgcgctcggc 60
gccgggagcg cggccagccg agtccggagg catcgggagg tcgagagccg ccgggacccc 120
agctctgcgt tcactgcccc gtccggagct ggacttcggg gccggggccg gggccgtgcg 180
ccggggacag gcagggccgg gtcgcgggcc gcgcgtcccc caggccggag atctgcgagt 240
gaagagggac aagggaaaag aaacaaagcc acagacgcaa cttgagactc ccgcatccca 300
aaagaagcac cagatcagca aaaaaagaag atgggccccc cgagcctcgt gctgtgcttg 360
ctgtccgcaa ctgtgttctc cctgctgggt ggaagctcgg ccttcctgtc gcaccaccgc 420
ctgaaaggca ggtttcagag ggaccgcagg aacatccgcc ccaacatcat cctggtgctg 480
acggacgacc aggatgtgga gctgggttcc atgcaggtga tgaacaagac ccggcgcatc 540
atggagcagg gcgggacgca cttcatcaac gccttcgtga ccacacccat gtgctgcccc 600
tcacgctcct ccatcctcac cggcaagtac gtccacaacc acaacaccta caccaacaat 660
gagaactgct cctcgccctc ctggcaggca cagcacgaga gccgcacctt tgccgtgtac 720
ctcaatagca ctggctaccg gacagctttc ttcgggaagt atcttaatga atacaacggc 780
tcctacgtgc cacccggctg gaaggagtgg gtcggactcc ttaaaaactc ccgcttttat 840
aactacacgc tgtgtcggaa cggggtgaaa gagaagcacg gctccgacta ctccaaggat 900
tacctcacag acctcatcac caatgacagc gtgagcttct tccgcacgtc caagaagatg 960
tacccgcaca ggccagtcct catggtcatc agccatgcag ccccccacgg ccctgaggat 1020
tcagccccac aatattcacg cctcttccca aacgcatctc agcacatcac gccgagctac 1080
aactacgcgc ccaacccgga caaacactgg atcatgcgct acacggggcc catgaagccc 1140
atccacatgg aattcaccaa catgctccag cggaagcgct tgcagaccct catgtcggtg 1200
gacgactcca tggagacgat ttacaacatg ctggttgaga cgggcgagct ggacaacacg 1260
tacatcgtat acaccgccga ccacggttac cacatcggcc agtttggcct ggtgaaaggg 1320
aaatccatgc catatgagtt tgacatcagg gtcccgttct acgtgagggg ccccaacgtg 1380
gaagccggct gtctgaatcc ccacatcgtc ctcaacattg acctggcccc caccatcctg 1440
gacattgcag gcctggacat acctgcggat atggacggga aatccatcct caagctgctg 1500
gacacggagc ggccggtgaa tcggtttcac ttgaaaaaga agatgagggt ctggcgggac 1560
tccttcttgg tggagagagg caagctgcta cacaagagag acaatgacaa ggtggacgcc 1620
caggaggaga actttctgcc caagtaccag cgtgtgaagg acctgtgtca gcgtgctgag 1680
taccagacgg cgtgtgagca gctgggacag aagtggcagt gtgtggagga cgccacgggg 1740
aagctgaagc tgcataagtg caagggcccc atgcggctgg gcggcagcag agccctctcc 1800
aacctcgtgc ccaagtacta cgggcagggc agcgaggcct gcacctgtga cagcggggac 1860

tacaagctca gcctggccgg acgccggaaa aaactcttca agaagaagta caaggccagc 1920
tatgtccgca gtcgctccat ccgctcagtg gccatcgagg tggacggcag ggtgtaccac 1980
gtaggcctgg gtgatgccgc ccagccccga aacctcacca agcggcactg gccaggggcc 2040
cctgaggacc aagatgacaa ggatggtggg gacttcagtg gcactggagg ccttcccgac 2100
tactcagccg ccaaccccat taaagtgaca catcggtgct acatcctaga gaacgacaca 2160
gtccagtgtg acctggacct gtacaagtcc ctgcaggcct ggaaagacca caagctgcac 2220
atcgaccacg agattgaaac cctgcagaac aaaattaaga acctgaggga agtccgaggt 2280
cacctgaaga aaaagcggcc agaagaatgt gactgtcaca aaatcagcta ccacacccag 2340
cacaaaggcc gcctcaagca cagaggctcc agtctgcatc ctttcaggaa gggcctgcaa 2400
gagaaggaca aggtgtggct gttgcgggag cagaagcgca agaagaaact ccgcaagctg 2460
ctcaagcgcc tgcagaacaa cgacacgtgc agcatgccag gcctcacgtg cttcacccac 2520
gacaaccagc actggcagac ggcgcctttc tggacactgg ggcctttctg tgcctgcacc 2580
agcgccaaca ataacacgta ctggtgcatg aggaccatca atgagactca caatttcctc 2640
ttctgtgaat ttgcaactgg cttcctagag tactttgatc tcaacacaga cccctaccag 2700
ctgatgaatg cagtgaacac actggacagg gatgtcctca accagctaca cgtacagctc 2760
atggagctga ggagctgcaa gggttacaag cagtgtaacc cccggactcg aaacatggac 2820
ctgggactta aagatggagg aagctatgag caatacaggc agtttcagcg tcgaaagtgg 2880
ccagaaatga agagaccttc ttccaaatca ctgggacaac tgtgggaagg ctgggaaggt 2940
taagaaacaa cagaggtgga cctccaaaaa catagaggca tcacctgact gcacaggcaa 3000
tgaaaaacca tgtgggtgat ttccagcaga cctgtgctat tggccaggag gcctgagaaa 3060
gcaagcacgc actctcagtc aacatgacag attctggagg ataaccagca ggagcagaga 3120
taacttcagg aagtccattt ttgcccctgc ttttgctttg gattatacct caccagctgc 3180
acaaaatgca ttttttcgta tcaaaaagtc accactaacc ctcccccaga agctcacaaa 3240
ggaaaacgga gagagcgagc gagagagatt tccttggaaa tttctcccaa gggcgaaagt 3300
cattggaatt tttaaatcat aggggaaaag cagtcctgtt ctaaatcctc ttattctttt 3360
ggtttgtcac aaagaaggaa ctaagaagca ggacagaggc aacgtggaga ggctgaaaac 3420
agtgcagaga cgtttgacaa tgagtcagta gcacaaaaga gatgacattt acctagcact 3480
ataaaccctg gttgcctctg aagaaactgc cttcattgta tatatgtgac tatttacatg 3540
taatcaacat gggaactttt aggggaacct aataagaaat cccaattttc aggagtggtg 3600
gtgtcaataa acgctctgtg gccagtgtaa aagaaaatcc ctcgcagttg tggacatttc 3660
tgttcctgtc cagataccat ttctcctagt atttctttgt tatgtcccag aactgatgtt 3720
ttttttttaa ggtactgaaa agaaatgaag ttgatgtatg tcccaagttt tgatgaaact 3780
gtatttgtaa aaaaaatttt gtagtttaag tattgtcata cagtgttcaa aaccccagcc 3840
aatgaccagc agttggtatg aagaaccttt gacattttgt aaaaggccat ttctttcttg 3900
ggagtttttt ggtgtgtctg ttttttaaa gtattcaaga tactaccagt caacatcttt 3960
ttggaagaaa atgccttggg tttagaagat tttcttaaaa ggggagtaga tggttgtaga 4020
ttgactaaaa agtctaccat acttcaaggg actacaggta agtctcatag tataccagct 4080
ttggtacttc atttttaaa aaagtattaa tcaattgcaa agaaattcgc cttggccaac 4140
ccttctttgt gtatcaggta gtctaacctg atacaagtag ttgacagatt tcaactatca 4200
atcaccagtc caacccattt ctcatttaac agatgacgga gataatccct aaaagcaccc 4260
acatttgttt caatgcccca aacaggccaa ggctccctag caactcccta gtggcgtttt 4320
ttaacttctc agaaactgtt accattattt gaaataggct tccttaacct cctttaccct 4380
taacccaaca gggattt 4397

<210> 12
<211> 885
<212> PRT

<213> Homo sapiens

<400> 12

Asp Ser Arg Ile Pro Lys Glu Ala Pro Asp Gln Gln Lys Lys Lys Met
1 5 10 15

Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe Ser
20 25 30

Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Leu Lys Gly
35 40 45

Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn Ile Ile Leu Val
50 55 60

Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Met Gln Val Met Asn
65 70 75 80

Lys Thr Arg Arg Ile Met Glu Gln Gly Gly Thr His Phe Ile Asn Ala
85 90 95

Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Ile Leu Thr
100 105 110

Gly Lys Tyr Val His Asn His Asn Thr Tyr Thr Asn Asn Glu Asn Cys
115 120 125

Ser Ser Pro Ser Trp Gln Ala Gln His Glu Ser Arg Thr Phe Ala Val
130 135 140

Tyr Leu Asn Ser Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
145 150 155 160

Asn Glu Tyr Asn Gly Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val
165 170 175

Gly Leu Leu Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn
180 185 190

Gly Val Lys Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr
195 200 205

Asp Leu Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys
210 215 220

Met Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro
225 230 235 240

His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro Asn
245 250 255

Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Pro Asp
260 265 270

Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro Ile His Met
275 280 285

Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
290 295 300

Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met Leu Val Glu Thr Gly
305 310 315 320

Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr His
325 330 335

Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Glu Phe
340 345 350

Asp Ile Arg Val Pro Phe Tyr Val Arg Gly Pro Asn Val Glu Ala Gly
355 360 365

Cys Leu Asn Pro His Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
370 375 380

Leu Asp Ile Ala Gly Leu Asp Ile Pro Ala Asp Met Asp Gly Lys Ser
385 390 395 400

Ile Leu Lys Leu Leu Asp Thr Glu Arg Pro Val Asn Arg Phe His Leu
405 410 415

Lys Lys Lys Met Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg Gly
420 425 430

Lys Leu Leu His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu Glu
435 440 445

Asn Phe Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg Ala
450 455 460

Glu Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys Val
465 470 475 480

Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro Met
485 490 495

Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr Tyr
500 505 510

Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys Leu
515 520 525

Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Lys Tyr Lys Ala
530 535 540

Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val Asp
545 550 555 560

Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg Asn
565 570 575

Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp Lys
580 585 590

Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser Ala
595 600 605

Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn Asp
610 615 620

Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp Lys
625 630 635 640

Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn Lys
645 650 655

Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg Pro
660 665 670

Glu Glu Cys Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys Gly
675 680 685

Arg Leu Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly Leu
690 695 700

Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys
705 710 715 720

Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys Ser
725 730 735

Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln Thr
740 745 750

Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala Asn
755 760 765

Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn Phe
770 775 780

Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu Asn
785 790 795 800

Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg Asp
805 810 815

Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Lys
820 825 830

Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly Leu
835 840 845

Lys Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg Lys
850 855 860

Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu Trp
865 870 875 880

Glu Gly Trp Glu Gly
885